

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 1, 2001, 16:16:52 ; Search time 91.75 Seconds
(without alignments)
21.119 Million cell updates/sec

Title: US-09-331-631A-7_COPY_81_140
Perfect score: 342
Sequence: 1 LQROYQQCQGRCORQQGQR.....HENYHNHKKNRSEEEGQQR 60

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Swissprot;39;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

8. SUMMARIES

RESULT	1	ALIGNMENTS	
RP	VCL_A_GOSHI	STANDARD;	PRT; 605 AA.
RA	VCL_A_GOSHI		
AC	P09799;		
DT	01-MAR-1989	(Rel. 10, Created)	
DT	01-MAR-1989	(Rel. 10, Last sequence update)	
DT	15-JUL-1999	(Rel. 38, Last annotation update)	
DE	VICILIN GC72-A PRECURSOR (ALPHA-GLOBULIN A).		
OS	Gossypium hirsutum (Upland cotton).		
OT	Eukaryota; Embryophyta; Tracheophyta; Spermatophyta;		
OC	Magnoliophyta; eudicots; core eudicots; Rosidae; eurosids II;		
OC	Malvales; Malvaceae; Gossypium.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Chian C.A., Borroto K., Kamalay J.A., Dure L. III;		
AC	"Developmental biochemistry of cottonseed embryogenesis and germination - XIX. Sequences and genomic organization of the alpha globulin (vicilin) genes of cottonseed.";		
CC	globulin (vicilin) genes of cottonseed.";		
RL	Plant Mol. Biol. 9:533-545(1987).		
CC	-- FUNCTION: SEED STORAGE PROTEIN.		
CC	-- SURCELLULAR LOCATION: COTYLEDONARY MEMBRANE-BOUND VACUOLAR PROTEIN BODIES.		
CC	-- SIMILARITY: TO OTHER 'S SEED STORAGE PROTEINS (PHASEOLIN, VICILIN, CONVICILIN, CONGLYCIIN, ETC.).		
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CC	--		
DR	EMBL; M19378; AAA33069.1; -.		
DR	PIR; S05398; S05398.		
DR	HSSP; P50477; 10AX.		
DR	INTERPRO; IPR001113; -.		
DR	PPAM; PF00546; Seedstore_7's; 1.		
FT	SEQUENCE 605 AA; 71049 MW; C9DB9371C976953B CRC54;		
FT	SEED storage protein; Signal 1 23		
FT	SIGNAL 1		
FT	CHAIN 24		
FT	SEQUENCE 605 AA; 71049 MW; C9DB9371C976953B CRC54;		
Query	3 ROYQQCQGRCORQQGOREQQOCQRCWEQYKEQE-RGEHEN-YHHHKNNSEEEGQQR		
Match	38.9%; score 133; DB 1; Length 605;		
Best Local Similarity	43.3%; Pred. No. 5.5e-06;		
Matches	26; Conservative 14; Mismatches 18; Indels 2; Gaps 2;		
DB	120 KQFECQRCQWQEQPERKOCVKCREQEDPKGERENKWREREESDEBQQQR 179		
RESULT	2		
ID	VCL_A_GOSHI	STANDARD;	PRT; 588 AA.

CC MEMBRANE PROTEINS BY TRANSGLUTAMINASE, ALL THAT RESULTS IN THE
CC FORMATION OF AN INSOLUBLE ENVELOPE BENEATH THE PLASMA MEMBRANE.
CC -!- TISSUE SPECIFICITY: PRESENT IN KERATINOCTYES OF EPIDERMIS AND
CC OTHER STRATIFIED SQUAMOUS EPITHELIUM.

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EMBL; M2513; AAA35375.1; -.
DR HSSP; P80220; 1D1P.
DR INTERPRO; IPR00354; -.
DR PFAM; PF00904; Involutrin.
DR PROST1; PT00795; INVOLUCRIN; 1.
DR Keratinocyte; Repeat.
SQ SEQUENCE 544 AA; 63927 MW; 2A02ABA5E1499F9D CRC64;

Query Match 24.4%; Score 83.5; DB 1; Length 544;
Best Local Similarity 34.8%; Pred. No. 0.25; RT
Matches 23; Conservative 11; Mismatches 21; Indels 11; Gaps 3; RT
ID ANDR_HUMAN STANDARD; PRT; 919 AA.
AC P10275; RT
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE ANDROGEN RECEPTOR (DIHYDROTESTOSTERONE RECEPTOR).
GN AR OR NR3C4 OR DHTR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Cetartiodactyla; Hominidae; Homo.
RN 1] SEQUENCE FROM N.A.
RP MEDLINE=89112208; PubMed=3216866;
RX Lubahn D.B., Joseph D.R., Sar M., Tan J., Higgs H.N., Larson R.E.,
RA French F.S., Wilson E.M.;
RA "The human androgen receptor: complementary deoxyribonucleic acid
RT cloning, sequence analysis and gene expression in prostate.";
RL Mol. Endocrinol. 2:1265-1275(1988).
RN 12] SEQUENCE FROM N.A.
RP MEDLINE=90083304; PubMed=2594783;
RX Lubahn D.B., Brown T.R., Simental J.A., Higgs H.N., Migeon C.J.,
RA Wilson E.M., French F.S.;
RA "Sequence of the intron/exon junctions of the coding region of the
RT human androgen receptor gene and identification of a point mutation
in a family with complete androgen insensitivity.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:9534-9538(1989).
RN 13] SEQUENCE FROM N.A.
RP MEDLINE=90258935; PubMed=2342476;
RA Govindan M.V.;
RT "Specific region in hormone binding domain is essential for hormone
proc. Natl. Acad. Sci. U.S.A. 86:9534-9538(1989).
RN 14] SEQUENCE FROM N.A.
RP MEDLINE=90258935; PubMed=2342476;

RP SEQUENCE FROM N.A.
RC TISSUE=PROSTATE; RT
RX MEDLINE=89017168; PubMed=3174628;
RA Chang C., Kokontis J., Liao S.;
RT "Structural analysis of complementary DNA and amino acid sequences of
human and rat androgen receptors.";
RT Proc. Natl. Acad. Sci. U.S.A. 85:7211-7215(1988).
RN [5] SEQUENCE FROM N.A.
RP TISSUE=PROSTATE; RT
RX MEDLINE=89088900; PubMed=2911578;
RA Tilley W.D., Marcelli M., Wilson J.D., McPhaul M.J.;
RA "Characterization and expression of a cDNA encoding the human androgen
receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:327-331(1989).
RN [6] SEQUENCE FROM N.A.
RP TISSUE=PROSTATE; RT
RX MEDLINE=91155943; PubMed=2293020;
RA Marcelli M., Tilley W.D., Wilson C.M., Griffin J.E., Wilson J.D.,
RA McPhaul M.J.;
RT "Definition of the human androgen receptor gene structure permits the
termination of the receptor protein at amino acid residue 588 causes
RT complete androgen resistance.";
RL Mol. Endocrinol. 4:1105-1116(1990).
RN [7] SEQUENCE OF 189-919 FROM N.A.
RX MEDLINE=88178111; PubMed=33526;
RA Chang C., Kokontis J., Liao S.;
RT "Molecular cloning of human and rat complementary DNA encoding
RT androgen receptors.";
RL Science 240:324-326(1988).
RN [8] SEQUENCE OF 468-919 FROM N.A.
RP MEDLINE=88240407; PubMed=3377788;
RA Trapman J., Klaassen P., Kuiper G.G.J.M., van der Korput J.A.G.M.,
RA Faber P.W., van Rooij H.C.J., Geurts van Kessel A., Voorthorst M.M.,
RA Mulder E., Brinkmann A.O.;
RT "Cloning, structure and expression of a cDNA encoding the human
RT androgen receptor.";
RL Biochem. Biophys. Res. Commun. 153:241-248(1988).
RN [9] POLYMORPHISM OF POLY-GLN REGION.
RP MEDLINE=92220629; PubMed=1561105;
RA Sleddens H.F., Oostra B.A., Brinkmann A.O., Trapman J.;
RT "Trinucleotide repeat polymorphism in the androgen receptor gene
RT (AR).";
RL Nucleic Acids Res. 20:1427-1427(1992).
RN [10] POLYMORPHISM OF POLY-GLN REGION.
RP TISSUE=BLOOD;
RC
RA Lu J., Danielsen M.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
RN [11] VARIANTS SBMA IN POLY-GLN REGION.
RP MEDLINE=91287825; PubMed=2062380;
RA Spada A.R., Wilson E.M., Lubahn D.B., Harding A.E., Fischbeck K.H.;
RT "Androgen receptor gene mutations in X-linked spinal and bulbar
RT muscular atrophy.";
RL Nature 352:77-79(1991).
RN [12] REVIEW ON VARIANTS.
RP MEDLINE=95023089; PubMed=1937057;
RA Patterson M.N., Hughes L.A., Gottlieb B., Pinsky L.;
RT "The androgen receptor gene mutations database.";
RL Nucleic Acids Res. 22:3560-3562(1994).
RN [13] REVIEW ON VARIANTS.
RP MEDLINE=97169385; PubMed=9016528;
RA Gottlieb B., Trifiro M., Lumbruso R., Vasiliou D.M., Pinsky L.;
RT "The androgen receptor gene mutations database.";
RL Nucleic Acids Res. 25:158-162(1997).

